

GeneCore version 5.1.4\_P5-4579

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 11:15:29 ; Search time 196.545 Seconds  
 (without alignment(s))  
 263,532 Million cell updates/sec

Title: US-10-086-184-1

Perfect score: 23

Sequence: 1 aatacggtccggaggcgaaaac 23

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_GeneSeq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*

8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*

11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

AADI4572

ID AADI4572 standard; DNA; 40 BP.

XX

AC AADI4572;

XX

DT 01-NOV-2001 (first entry)

XX

DE Arabidopsis thaliana ABP binding sequence #19.

XX

KW Abscisic acid responsive element; ABRE; ABRE-binding factor; ABF;

KW stress treatment; transgenic plant; environmental stress; db.

XX

OS Arabidopsis thaliana.

XX

FH Key Location/Qualifiers

FT misc\_feature 19..29

FT /\*tag= a

FT /\*note= "Conserved region"

FT misc\_feature 29

FT /\*tag= b

/note= "S is present at this location in the sequence shown in column 43 of the specification"

Nerve mutation fac

XX

(KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.

Disclosure; Fig 5B; 37pp; English.

WPI; 2001-366358/3B.  
New nucleic acid encoding abscisic acid responsive element binding factor 4, useful for generating transgenic plants, which are tolerant to multiple environmental stresses - Disclosure; Fig 5B; 42pp; English.

The invention relates to nucleic acid encoding the Abscisic acid responsive element (ABRE)-binding factor 4 (ABF4). ABF4 belongs to the ABF family of factors which bind abscisic acid responsive elements in plants. Expression of ABFs is inducible by abscisic acid and various stress treatments. ABFs have the potential to activate a large number of abscisic acid/stress responsive genes and thus a nucleic acid molecule encoding ABF4 is useful for generating transgenic plants that are tolerant to multiple environmental stresses. The present sequence is *Arabidopsis thaliana* ABF binding sequence which contains the group IA consensus sequence.

The sequence represents an oligonucleotide studied in a binding site selection assay, for studying the abscisic acid responsive element binding factor (ABF) protein. The oligonucleotide contains the IA consensus sequence. ABFs are bZIP class transcription factors that can bind to two classes of ABREs, namely G-box-like ABREs ( $G/ABRE$ ) and coupling element-like ABREs ( $C/ABRE$ ). Expression of ABF is inducible by abscisic acid and various stress treatments and they can transactivate an ABRE-containing reporter gene in yeast. Therefore, the ABFs are useful for activating a large number of abscisic acid or stress responsive genes and for generating transgenic plants that are tolerant to multiple environmental stresses.

CC  
CC of abscisic acid/stress responsive genes and thus a nucleic acid  
molecule encoding ABP4 is useful for generating transgenic plants  
that are tolerant to multiple environmental stresses. The present  
sequence is *Arabidopsis thaliana* ABP binding sequence which contains  
the group IA consensus sequence.

Qy	Db
1 AAATCGGCTCGAGCGGGAAAC	23
2 AATTGCCTTAAGGGGGACAC	24

RESULT 2  
AAS07877 standard; DNA; 40 BP.  
ID AAS07877  
XX  
XX  
AC  
XX  
AAS07877;  
DT  
XX  
DE  
Binding site selection assay group IA sequence #19.

KW  
Abscisic acid -responsive element binding factor; ABF; bZIP; ss; GABRE; G-box-like ABRE; coupling element-like ABRE; C/ABRE; transgenic plant; stress responsive gene; environmental stress; cress; KW  
binding site selection assay.

OS	Synthetic.
XX	
FH	
FT	
FT	
key	Location/Qualifiers
misc_feature	20..29
	/ *tag= ^a
	/notes= "Group IA consensus sequence"

XX  
PN  
XX  
PD  
XX  
PF  
  
EP1097999-A2.  
09-MAY-2001.  
29-JUN-2000; 2000EP-0305459.

XX  
PR 04-NOV-1999;  
XX 99KR-0048477.  
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.  
XX PI Kim SY;  
XX DR WPI: 2001-33711/36.

XX  
PT Nucleic acid encoding novel transcription factors that bind to various  
PT abiotic acid responsive elements, for generating stress tolerant  
PT transgenic plants -

CC class transcription factors that bind to both G-box-like ABREs (G/ABREs) and coupling element like ABREs (C/ABRE). ABFs have the potential to activate a large number of abscisic acid/stress responsive genes, and are therefore used to generate transgenic plants that are tolerant to multiple environmental stresses.

CC The present DNA sequence is *Arabidopsis thaliana* ABF binding sequence which contains the group IA consensus sequence.

CC Note: This sequence is stated to be the same as that shown as SEQ ID NO: 51 in the sequence listing of the specification. However the sequences differ at position 29.

SQ Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;

Query Match 65.2%; Score 15; DB 22; Length 40;  
Best Local Similarity 78.3%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATCGCTCGAGGGGGAAC 23  
Db 2 ATTCGCCTTAAGGGGACAC 24

RESULT 4

AAS0391 AAAS0391 standard; DNA; 40 BP.  
XX AAS0391;

DT 29-AUG-2001 (first entry)

DE A group IA abscisic acid response element (G/ABRE).  
XX KW Abscisic acid response element; G/ABRE; ABRE binding factor; ABF; transgenic plant; stress responsive gene; environmental stress response; probe; ds; G-box.

XX OS Synthetic.

XX PH Key `protein\_bind Location/Qualifiers  
PT 19..27  
PT /\*tgg= a  
PT /bound\_moiety= "ABF"

XX PN US6218527-B1.  
XX PD 17-APR-2001.  
XX PR 19-SEP-2000; 2000US-0664800.

XX PR 12-OCT-1999; 99US-0416050.

XX PR 12-OCT-1999; 99US-0416050.

XX PR WPI; 2001-217937/22.

XX PT New nucleic acid molecule encoding Abscisic acid responsive element binding factor 1 (Abf1) which can be used to generate transgenic plants that are tolerant to multiple environmental stresses -

XX DS disclosure; Fig 5B; 42pp; English.

XX CC The sequence represents the ABRE binding sequence 45, identified from binding site selection analysis of abscisic acid responsive element binding factors (ABFs), isolated from an *Arabidopsis* cDNA library. CC Abscisic acid (ABA) is a major plant hormone involved in response to adverse environmental conditions such as drought, high salt and cold/ freezing. This response involves induced expression of various genes. CC ABBA-responsive elements (ABREs) are cis-regulatory elements that mediate CC the ABA-modulated gene expression, and interact with a novel class of CC ABRE-binding factors (ABFs). ABFs are basic leucine zipper (bZIP) class CC transcription factors that bind to both G/ABREs and C/ABREs. ABFs have CC the potential to activate a large number of ABA/stress responsive genes CC and can be used to generate transgenic plants that are tolerant to multiple environmental stresses.

XX SQ Sequence 40 BP; 9 A; 11 C; 12 G; 7 T; 1 other;  
Query Match 65.2%; Score 15; DB 22; Length 40;  
Best Local Similarity 78.3%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 AAATGGCTCGAGGGGGAAC 23  
Db 2 ATTCGCCTTAAGGGGACAC 24

XQ Sequence 40 BP; 9 A; 11 C; 12 G; 7 T; 1 other;

Query Match 65.2%; Score 15; DB 22; Length 40;  
Best Local Similarity 78.3%; Pred. No. 8e+02; Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATCGCTCGAGGGGGAAC 23  
Db 2 ATTCGCCTTAAGGGGACAC 24

RESULT 5

AAS0410 ID AAS0410 standard; cDNA; 40 BP.  
XX AC AAS0410;

DT 25-MAY-2001 (first entry)

XX DE ABRE binding sequence 45, identified from binding site selection.

XX KW Abscisic acid responsive element binding factor 1; Abf1; plant hormone; drought; ABA-responsive element; ABRE; ABRE-binding factor; ABF; basic leucine zipper; bZIP; G/ABRE; C/ABRE; transgenic plant; environmental stress; ss.

XX OS *Arabidopsis thaliana*.

XX PN US6194559-B1.

XX PD 27-FEB-2001.

XX PR 12-OCT-1999; 99US-0416050.

XX PR 12-OCT-1999; 99US-0416050.

XX PR (KOKU-) KORBA KUMHO PETROCHEMICAL CO LTD.

XX PI Kim SY;

XX DR WPI; 2001-217937/22.

XX PT New nucleic acid molecule encoding Abscisic acid responsive element binding factor 1 (Abf1) which can be used to generate transgenic plants that are tolerant to multiple environmental stresses -

XX DS disclosure; Fig 5B; 42pp; English.

XX CC The sequence represents the ABRE binding sequence 45, identified from binding site selection analysis of abscisic acid responsive element binding factors (ABFs), isolated from an *Arabidopsis* cDNA library. CC Abscisic acid (ABA) is a major plant hormone involved in response to adverse environmental conditions such as drought, high salt and cold/ freezing. This response involves induced expression of various genes. CC ABBA-responsive elements (ABREs) are cis-regulatory elements that mediate CC the ABA-modulated gene expression, and interact with a novel class of CC ABRE-binding factors (ABFs). ABFs are basic leucine zipper (bZIP) class CC transcription factors that bind to both G/ABREs and C/ABREs. ABFs have CC the potential to activate a large number of ABA/stress responsive genes CC and can be used to generate transgenic plants that are tolerant to multiple environmental stresses.

CC The sequence represents a group IA G-box containing abscisic acid response element (G/ABRE), used in a gel mobility shift assay, testing for the binding of ABRE binding factor, ABF1. The nucleic acid encoding an ABF can be used to generate transgenic plants that are tolerant to multiple environmental stresses e.g. drought, high salt, and cold/ freezing. Expression of the binding factor is inducible by abscisic acid and various stress treatments, and can transactivate an abscisic acid responsive element (ABRE)-containing a reporter gene in yeast. The binding factor can activate a number of abscisic acid/stress responsive genes.

**RESULT 6**  
 AAH4735/C  
 ID AAH4735 standard; DNA; 18 BP.  
 XX  
 AC AAH4735;  
 XX  
 DT 30-NOV-2001 (first entry)  
 DE Human Her-3 mRNA inhibiting antisense oligo ISIS # 19550.  
 XX  
 KW Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;  
 XX  
 KW antiinflammatory; cytostatic; antibacterial; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US6277640-B1.  
 XX  
 PD 21-AUG-2001.  
 XX  
 PR 31-JUL-2000; 2000US-0630706.  
 XX  
 PR 31-JUL-2000; 2000US-0630706.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PT Bennett CF, Cowpert LM;  
 XX  
 DR WPI; 2001-535134/59.  
 XX  
 PS Claim 1; Column 42; 49pp; English.  
 XX  
 PT Antisense compounds capable of modulating expression of human Her-3,  
 PT member of epidermal growth factor family of receptor/tyrosine kinases,  
 PT useful for preventing or delaying infection, inflammation or tumor  
 PT formation -  
 XX  
 PS The invention provides antisense compounds capable of inhibiting the  
 CC expression of human Her-3, a member of epidermal growth factor (EGF)  
 CC family of receptor/tyrosine kinases. The antisense oligonucleotides are  
 CC useful for inhibiting the expression of Her-3 in cells or tissues. They  
 CC are commonly used as research reagents and in diagnostics for example, to  
 CC elucidate the function of particular genes. The antisense compounds are  
 CC also useful for distinguishing between functions of various members of a  
 CC biological pathway and for research use. They are also utilized for  
 CC diagnostics, therapeutics, prophylaxis and in kits. They are useful  
 CC prophylactically, e.g. to prevent or delay infection, inflammation or  
 CC tumor formation. Sequences AAH4732-7615 represent chimeric antisense  
 CC phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,  
 CC used for the inhibition of Her-3 mRNA expression.  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 other;

Query Match 64.3%; Score 14.8; DB 22; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 9.5e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GCGTCCGAGGCCGGAAAC 23  
 Db 18 GGCGCCGAGGTGGCAAC 1

**RESULT 7**  
 AX06374/C  
 ID AX06374 standard; DNA; 31 BP.  
 AC AX06374;  
 XX  
 DT 31-MAR-1999 (first entry)  
 XX  
 DE Human biallelic polymorphic DNA fragment SCG33319.

Query Match 63.5%; Score 14.6; DB 20; Length 31;  
 Best Local Similarity 73.9%; Pred. No. 1.2e+03;  
 Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATCGCTCGAGGGGAAC 23  
 Db 30 ACATCAGTCACGKCTGAAAC 8

**RESULT 8**  
 AAC73135/C  
 ID AAC73135 standard; DNA; 38 BP.  
 AC AAC73135;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE Single base extension primer #16 used in multiplexing PCR/SBE assay.  
 XX  
 KW Oligonucleotide array; genotyping; single base extension reaction; SBE;  
 KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200058516-A2.  
 PD 05-OCT-2000.

XX  
PP 27-MAR-2000; 2000WO-US08069.  
XX  
PR 26-MAR-1999; 99US-012473.  
XX 23-JUN-1999; 99US-0140359.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (AFFY-) AFFYMATRIX INC.  
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;  
PI Ryder T, Sklar P;  
XX DR WPI; 2000-656171/63.  
XX PT Universal array of oligonucleotides tags attached to a solid substrate comprising  
PT along with locus-specific tagged oligonucleotides useful in genotyping  
PT using single base extension reactions -  
XX Example 7; Page 49; 83pp; English.  
XX CC The present invention relates to an oligonucleotide array comprising  
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide  
CC array is useful for genotyping a nucleic acid sample at one or more loci  
CC via single base extension (SBE) reactions. A pair of primers is used to  
CC amplify a polymorphic locus in a sample e.g. a single nucleotide  
CC polymorphism (SNP). The amplified nucleic acid product is then used as a  
CC template in a SBE reaction with an extension primer. The present sequence  
CC is one such SBE reaction primer used in the method of the present  
CC invention. The SBE reaction products are used to form the oligonucleotide  
CC array.  
XX SQ Sequence 38 BP; 7 A; 13 C; 10 G; 8 T; 0 other:  
Query Match 61.7%; Score 14.2; DB 21; Length 38;  
Best Local Similarity 84.2%; Pred. No. 1.9e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CC QY 4 TCGGGCTCCGAGGCCGAA 22  
Db 36 TCGGCTCCGAGGTCGAAGA 18  
XX OS RESULT 9  
ID AAX77145/c standard; DNA; 23 BP.  
XX AC AAX77145;  
XX DT 03-AUG-1999 (first entry)  
DE Nerve mutation factor DNA amplifying primer.  
XX KW Nerve mutation factor; chromosome 10; glioma; tumour suppressor;  
KW brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.  
XX KW brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.  
KW minimal DNA binding element; ss.  
XX OS Synthetic.  
XX KEY Location/Qualifiers  
FT misc\_feature 1.17  
FT misc\_feature /\*tag= a  
FT misc\_feature /note= "contact sequence"  
FT misc\_feature 1 /\*tag= b  
FT misc\_feature /note= "contact point"  
FT misc\_feature 5 /\*tag= c  
FT misc\_feature /note= "contact point"  
FT misc\_feature 6 /\*tag= d  
FT misc\_feature /note= "contact point"  
FT misc\_feature 7 /\*tag= e  
FT misc\_feature /note= "contact point"  
FT misc\_feature 9 /\*tag= f  
FT misc\_feature /note= "contact point"  
FT misc\_feature 10 /\*tag= g  
FT misc\_feature /note= "contact point"  
FT misc\_feature 12 /\*tag= h  
FT misc\_feature /note= "contact point"  
FT misc\_feature 14 /\*tag= i  
FT misc\_feature /note= "contact point"  
FT misc\_feature 17 /\*tag= j  
XX Nakamura H, Nakata M, Saya H, Yoshida M;  
XX WPI; 1999-3474/29.  
XX Human gene on chromosome 10 homologous to Drosophila neuralized  
gene, useful in the diagnosis and gene therapy of brain tumors

XX Examples; Page 24; 78pp; Japanese.  
XX  
The invention relates to a protein which is a nerve mutation factor and  
CC is the expression product of a gene located on chromosome 10. The gene  
CC is in a region frequently deleted in highly malignant gliomas. Sequences  
CC (AAY77135 and AAY77136) encoding human and mouse nerve mutation factors  
CC (AAY21558 and AAY21559) are provided. The protein is believed to have  
CC tumour suppressor activity. Polynucleotide sequences and antibodies to  
CC the protein are diagnostic reagents for highly malignant brain tumors  
CC such as astrocytoma where chromosome 10 deletion commonly occurs. The  
CC gene may also be used for gene therapy of such tumors.  
XX SQ Sequence 23 BP; 2 A; 8 C; 8 G; 5 T; 0 other:  
Query Match 60.0%; Score 13.8; DB 20; Length 23;  
Best Local Similarity 88.2%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
ID AAT08994/c  
ID AAT08994 standard; DNA; 26 BP.  
XX AC AAT08994;  
XX DT 25-JUL-1996 (first entry)  
XX DE Insulin response element A minimal DNA binding element.  
XX KW Insulin response element A; IRE-A; E2F; liver IRP-A;  
KW Rb-associated protein; RBAP-1; E2F-1; rapamycin; inhibition;  
KW insulin-induced; expression; carbohydrate uptake;  
KW triglyceride biosynthesis; treatment; prevention; obesity;  
KW type II diabetes mellitus; insulin dependent tumours;  
KW minimal DNA binding element; ss.  
XX OS Synthetic.  
XX KEY Location/Qualifiers  
FT misc\_feature 1.17  
FT misc\_feature /\*tag= a  
FT misc\_feature /note= "contact sequence"  
FT misc\_feature 1 /\*tag= b  
FT misc\_feature /note= "contact point"  
FT misc\_feature 5 /\*tag= c  
FT misc\_feature /note= "contact point"  
FT misc\_feature 6 /\*tag= d  
FT misc\_feature /note= "contact point"  
FT misc\_feature 7 /\*tag= e  
FT misc\_feature /note= "contact point"  
FT misc\_feature 9 /\*tag= f  
FT misc\_feature /note= "contact point"  
FT misc\_feature 10 /\*tag= g  
FT misc\_feature /note= "contact point"  
FT misc\_feature 12 /\*tag= h  
FT misc\_feature /note= "contact point"  
FT misc\_feature 14 /\*tag= i  
FT misc\_feature /note= "contact point"  
FT misc\_feature 17 /\*tag= j  
XX Nakamura H, Nakata M, Saya H, Yoshida M;  
XX WPI; 1999-3474/29.  
XX Human gene on chromosome 10 homologous to Drosophila neuralized  
gene, useful in the diagnosis and gene therapy of brain tumors

PT /notes= "contact point"  
 PT XX  
 PN WO9531104-A1.  
 XX  
 PD 23-NOV-1995.  
 XX  
 PF 10-MAY-1995; 95WO-US05835.  
 PR 13-MAY-1994; 94US-0242409.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PT Alexander-Bridges MC, Zhao H;  
 XX DR  
 XX  
 PT Use of rapamycin to inhibit insulin-induced adiposis - for treating  
 PT insulin-induced obesity, weight gain and other conditions associated  
 PT with hyperinsulinaemia  
 XX WPI; 1996-049292/05.  
 XX  
 PS Example; Page 27; 55pp; English.

XX  
 CC The present sequence is the insulin response element A (IRE-A)  
 CC minimal DNA binding element, which binds, with identical contact  
 CC sequence contact points, to liver IRE-A, and the cloned  
 CC Rb-associated protein RBAP-1 (E2F-1). This information was used in  
 CC the development of the invention, i.e. rapamycin inhibition of  
 CC insulin-induced expression of carbohydrate uptake, and  
 CC triglyceride biosynthesis genes useful in the treatment and  
 CC prevention of obesity, type II diabetes mellitus and insulin  
 CC dependent tumours, etc..  
 XX  
 SQ Sequence 26 BP; 4 A; 10 C; 4 G; 8 T; 0 other;

Query Match 60.0%; Score 13.8; DB 17; length 26;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GCCTCCGAGGGAAA 22  
 Db 18 GGCTGAGAGGGAA 2

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RESULT 11  
 ART5155  
 ID ART5155 standard; DNA; 29 BP.  
 XX  
 AC AC  
 AC ART5155;  
 AC  
 DT 18-AUG-1997 (first entry)

DE Homeoprotein regulator of insulin gene expression primer GST-GGGS.  
 XX  
 KW Antibody; diabetes; breast cancer; insulin dependent diabetes;  
 KW hypoglycaemia; hyperglycaemia; polymerase chain reaction; ss.  
 OS Synthetic.  
 XX  
 PN WO9636711-A2.  
 PD 21-NOV-1996.  
 XX  
 PP 09-MAY-1996; 96WO-US06608.  
 XX  
 PR 09-MAY-1995; 95US-0437607.  
 XX  
 PA (SALK ) SALK INST.  
 PA (STRA-) STRANG CANCER PREVENTION CENT.  
 XX  
 PI Leonard JN, Montminy MR;  
 XX  
 DR WPI; 1997-012086/01.  
 XX

---

PT New homeo:protein regulator of insulin gene expression - and related  
 PT DNA and antibodies, useful for detecting e.g diabetes or breast  
 PT cancer;  
 XX  
 PS Examples; Page 44; 96pp; English.

XX  
 CC The present sequence is primer GST-GGGS used in the examples in order  
 CC to more fully illustrate the preferred embodiments of the invention.  
 CC The HoxB13 gene encodes a homeoprotein regulator of insulin gene  
 CC expression. The novel homeoprotein regulator of insulin gene expression  
 CC is a protein (or its active fragments, agonists and/or mimics) which  
 CC binds the FLAT element of an insulin gene promoter; which is modulated  
 CC by a Ca2+-dependent CAM kinase IV; and which is homologous to a sequence  
 CC encoded by a Hox gene complex. Detection of altered levels of the HoxB13  
 CC protein indicates a disease related to glucose homeostasis, particularly  
 CC (non-)insulin dependent diabetes, hypo- or hyper-glycaemia, or also  
 CC breast cancer. Antibodies are useful as reagents for immunoassays. The  
 CC protein and compounds that promote and inhibit its production or  
 CC activity or its specific binding partners, are useful for preventing or  
 CC treating the specified diseases, especially where insulin is also being  
 CC administrated.

XX  
 SQ Sequence 29 BP; 4 A; 9 C; 10 G; 6 T; 0 other;

Query Match 60.0%; Score 13.8; DB 18; Length 29;  
 Best Local Similarity 88.2%; Pred. No. 3e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CGGCTCGAGGGAAA 21  
 Db 3 CGGATCCGAGGGGTAA 19

---

RESULT 12  
 AAQ49298  
 ID AAQ49298 standard; DNA; 33 BP.  
 XX  
 AC AAQ49298;  
 AC  
 DT 28-APR-1994 (first entry)

DE Degenerin PCR primer.

XX  
 KW Long-distance homology; evolution; nematode;  
 KW hybridisation; lower organism; structural homologue;  
 KW Alzheimer's disease; cell death gene; PCR; polymerase chain reaction;  
 KW ciona intestinalis; echinoderm; lamprey; puffer fish;  
 KW mammal; probe; ss.  
 XX  
 OS Synthetic.

XX  
 PN WO9320237-A.

PD 14-OCT-1993.

XX  
 PF 01-APR-1993; 93WO-US03102.

PR 01-APR-1992; 92US-0861458.

XX  
 PA (CAMB-) CAMBRIDGE NEUROSCIENCE INC.

XX  
 PT Johnson CD, Marchionni MA;  
 XX  
 DR WPI; 1993-336943/42.

XX  
 PT Long-distance homology cloning of genes from lower organisms -  
 PT used to identify DNA that codes for evolutionary conserved  
 PT aminoacid sequences  
 XX  
 PS Disclosure; Fig 14; 188pp; English.

XX  
 CC The primers (AAQ49297-Q49348) and probes (AAQ49322-Q49348) are used to  
 CC isolate degenerin homologues from genomic DNA templates from three

CC nematodes; *Caenorhabditis elegans*, *C. briggsae*, *Ascaris suum*.  
 CC The primers were based on area I and II amino acid sequences common  
 CC to the degenerin gene family members DEG-1 and MBC-4 from *C. elegans*.  
 XX Sequence 33 BP; 6 A; 7 C; 9 G; 5 T; 6 other;

SQ Query Match 60.0%; Score 13.8; DB 14; Length 33;  
 Best Local Similarity 65.2%; Pred. No. 3e+03; Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAATGGCTCCGAGGGGGAAAC 23  
 Db 3 AATTCGGATCCGGNACNGGAA 25

RESULT 13  
 AAT08992/C  
 ID AAT08992 standard; DNA; 37 BP.  
 XX  
 AC AAT08992;  
 DT 25-JUL-1996 (first entry)  
 XX  
 DE Transfection analysis minimal binding motif.  
 XX  
 KW Insulin response element A; IRE-A; E2F; liver IRP-A;  
 KW Rb-associated protein; RbP-1; rapamycin; inhibition;  
 KW insulin-induced; expression; carbohydrate uptake;  
 KW triglyceride biosynthesis; treatment; prevention; obesity;  
 KW type II diabetes mellitus; insulin dependent tumors;  
 KW electrophoretic mobility shift assay; EMSA;  
 KW transfection analysis; minimal binding motif; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9466913-A.  
 XX  
 PD 31-MAR-1994.  
 XX  
 PP 17-SBP-1993; 93WO-US08849.  
 XX  
 PR 18-SBP-1992; 92US-0917263.  
 XX  
 PA (USSH ) US SEC DEPT HEALTH.  
 XX  
 PI Emerson SU, Purcell RH, Tsarev SA;  
 XX  
 DR WPI; 1994-118462/14.  
 XX  
 PT Purified hepatitis B strain SAR-55 virus - used to develop prods.  
 PT for use in detection, diagnosis, vaccines and therapy of  
 PT hepatitis B virus infection  
 XX  
 PS Example 1; Page 40; 114PP; English.

XX  
 CC The sequences given in AAQ45198-200 and AAQ01687-777 are primers which  
 CC were used in the isolation and amplification of the genomic sequence  
 CC of the hepatitis B Virus (HBV) strain SAR-55. These primers were  
 CC based on sequences derived from the SAR-55 strain and a strain from  
 CC Burma (BUR-121). The amplified sequence contains three open reading  
 CC frames (ORFs). The proteins encoded by this sequence can be used to  
 CC stimulate the production of protective antibodies upon injection into  
 CC a mammal that would serve to protect the mammal upon challenge with  
 CC wild type HBV. The proteins can be used for detection and diagnosis  
 CC of HBV infection. This cDNA was isolated from primates inoculated  
 CC with stool suspensions obtained from hepatitis B patients.  
 XX  
 SQ Sequence 29 BP; 6 A; 10 C; 9 G; 4 T; 0 other;

CC The present sequence is a transfection analysis minimal binding  
 CC motif, which was used in an electrophoretic mobility shift assay to  
 CC characterise insulin response element A (IRE-A) like and E2F like  
 CC binding activities. IRE-A normally binds, with identical contact  
 CC sequence contact points, to liver IRP-A, and the cloned  
 CC Rb-associated protein RBAP-1 (E2P-1). This information was used in  
 CC the development of the invention, i.e. rapamycin inhibition of  
 CC insulin-induced expression of carbohydrate uptake, and  
 CC triglyceride biosynthesis genes, useful in the treatment and  
 prevention of obesity, type II diabetes mellitus and insulin  
 CC dependent tumours, etc..  
 XX  
 SQ Sequence 37 BP; 8 A; 14 C; 5 G; 10 T; 0 other;

Query Match 60.0%; Score 13.8; DB 17; Length 37;  
 Best Local Similarity 88.2%; Pred. No. 3e+03; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCGGCTCCGAGGGGGAAAC 22  
 Db 8 ATCCGGCTCCAGGGCTCAA 27

RESULT 15  
 AT27471  
 ID AT27471 standard; DNA; 29 BP.  
 XX  
 AC AT27471;  
 XX  
 DT 27-NOV-1996 (first entry)  
 XX  
 DB HEV strain Burma-121 derived reverse primer 81 (ORF-1).

Page 8

**XX** Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;  
**KW** structural region; antigen; detection; antibody; vaccine;  
**KW** immunisation; infection; primer; Buurma-121;  
**KW** polymerase chain reaction; PCR; Aa

Synthetic.

11-APR-1996.

03-OCT-1994; 94US-0316765.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Emerson SU, Purcell  
WPI: 1996-209320/31.

Isolated and purified antigenic protein us

Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection

The Preagent Sectarianism is a heretical

derived primer, used in the isolation of the HEV strain SAR-55 from CDNA. The HEV strain SAR-55 was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded

by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors ppIC9-1779, -1780 and -1781.

Sequence 29 Bp; 6 A; 10 C; 9 G; 4 T; 0 other;

```

Query Match      59.1%; Score 13.6; DB 17; Length 29;
Best Local Similarity 80.0%; Prod. No. 3..7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0

```

	b	y
3	ATCGGCTCCGAGGGGAA	22
8	ATCCGCTCCAGCGTCAAA	27

search completed: March 26, 2003, 11:22:02  
Ob time : 197.545 BeCs